

FIGURE 1

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R35464	GGCCGGGTCG	TTTCTCGCCT	GGCTGGGATC	GCTGCTCCTC	TCTGGGGTCC	50
ORF	P	G	R	F	S	16
R35464	TGGCCGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	100
ORF	W	P	A	D	R	33
R35464	GGTGGTGGGC	AGATTCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	150
ORF	V	V	G	R	E	50
R35464	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	200
ORF	D	G	S	C	Q	66
R35464	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	250
ORF	N	N	Y	L	T	83
R35464	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCT	300
ORF	E	N	A	T	G	100
R35464	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CTTGAAGACC	ACTTCAGCGA	350
ORF	V	P	S	A	P	116
R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCAACGN	ATT-----	393
ORF	Y	V	S	*	I	130

KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)

ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

0021813.1229

FIGURE 2

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R74593	GCAATAATTA	CCTGACCAAG	GAGGAGTGCC	TCAAGAAATG	TGCCACTGTC	50
ORF	Q * L	P D Q G	G V P	Q E M	C H C H	17
R74593	ACAGAGAATG	CCACGGGTGA	CCTGGCCACC	AGCAGGAATG	CAGCGGATTC	100
ORF	R E C	H G *	P G H Q	Q E C	S G F	33
R74593	CTCTGTCCCA	AGTCTCCCAG	AAGGCAGGAT	TCTGAAGACC	ACTCCAGCGA	150
ORF	L C P K	S P R	R Q D	S E D H	S S D	50
R74593	TATGTTCAAC	TATGAAGAAT	ACTGCACCGC	CAACGCAGTC	ACTGGGCCTT	200
ORF	M F N	Y E E Y	C T A	N A V	T G P C	67
R74593	GCCGTGCATC	CTTCCCACGC	TGGTACTTTG	ACGTGGAGAG	GAACTCCTGC	250
ORF	R A S	F P R	W Y F D	V E R	N S C	83
R74593	AATAACTTCA	TCTATGGAGG	CTGCCGGGGC	AATAAGAACA	GCTACCGCTC	300
ORF	N N F I	Y G G	C R G	N K N S	Y R S	100
R74593	TGAGGAGGCC	TGCATGCTCC	GCTGCTTCCG	CCAGCAGGAG	AATCCTCCCC	350
ORF	E E A	C M L R	C F R	Q Q E	N P P L	117
R74593	TGCCCCTTGG	CTCAAAGGTG	GTGGTTCTGG	CCGGGGCTGT	TTCGTGATGG	400
ORF	P L G	S K V	V V L A	G A V	S * W	133
R74593	TGTTGATCCT	TTTCCTGGGG	AGCNTCCATG	GTCTTACTGA	TTCCGGGTGG	450
ORF	C * S F	S W G	A S M	V L L I	P G G	150
R74593	CAAGGAGGAA	CCAGGAGCGT	GCCCTGCGGA	NCGTCTGGAG	CTTCGGAGAT	500
ORF	K E E	P G A C	P A X	R L E	L R R *	167
R74593	GACAAGGGNT					510
ORF	Q G					169

KEY

R74593 = Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)

ORF = EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

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FIGURE 3

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R35464	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50
N39798			TGGGANTC	GCTGCTCCTC	TCTGGGGTCC	28
H94519	GCNGCG-CGT	TNNTCGCNT-	GCTGGGA-TC	GCTGCACCTC	TCTGGGGTCC	47
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	GGCCGGGTCGT	TTCTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC	50
Translation	A G S F	L A W	L G S	L L L	S G V	-3
R35464	TGGCCGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	100
N39798	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	77
H94519	NGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	96
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	TGG-CGGCCG	ACCGAGAACG	CAGCATCCAC	GACTTCTGCC	TGGTGTGCGAA	99
Translation	L A A D	B E B	S I H	D E C L	Y S K	15
R35464	GGTGGTGGGC	AGATTCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	150
N39798	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	127
H94519	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	146
R74593 corr.	-----	-----	-----	-----	-----	
Consensus	GGTGGTGGGC	AGATGCCGGG	CCTCCATGCC	TAGGTGGTGG	TACAATGTCA	149
Translation	Y Y G	B C B A	S M R	B H H	X N Y Z	32
R35464	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	200
N39798	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	177
H94519	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	196
R74593 corr.	-----	-----	-----	-----	-----GC	2
Consensus	CTGACGGATC	CTGCCAGCTG	TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC	199
Translation	D G S	C Q L	E Y Y G	G C D	G N S	48
R35464	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	250
N39798	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	227
H94519	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	246
R74593 corr.	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	52
Consensus	AATAATTACC	TGACCAAGGA	GGAGTGCCTC	AAGAAATGTG	CCACTGTCAC	249
Translation	N N Y L	T K E	E C L	K K C A	T V T	65
R35464	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	300
N39798	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	277
H94519	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	296
R74593 corr.	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	102
Consensus	AGAGAATGCC	ACGGGTGACC	TGGCCACCAG	CAGGAATGCA	GCGGATTCCCT	299
Translation	E N A	T G D L	A T S	R N A	A D S S	92
R35464	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CTTGAAGACC	ACTTCAGCGA	350
N39798	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	326
H94519	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	345
R74593 corr.	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	151
Consensus	CTGTCCCAAG	TGCTCCCAGA	AGGCAGGATT	CT-GAAGACC	ACTCCAGCGA	348
Translation	V P S	A P R	R Q D S	E D H	S S D	98
R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCAACGN	ATT-----	393
N39798	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	372
H94519	TATGTT-CAA	CTA-TG-AAG	AATACTGGCA	CCGCCAACGC	ATTCACTGGG	392
R74593 corr.	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	197
Consensus	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	394
Translation	M F N	Y E E	Y C T	A N A	V T G	113

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FIGURE 3 (CONT)

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R35464	-----	-----	-----	-----	-----	
N39798	CCTTGC-GTG	GAATCCTTTC	CCACGCTGGN	AATTTNGACG	TTGAGAAGGA	421
H94519	CCT-GC-GTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GNCG	-----	427
R74593 corr.	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	243
Consensus	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	440
Translation	P C R A	S F	P R W Y	F D V	E R N	129

R35464	-----	-----	-----	-----	-----	
N39798	AC-----	-----	-----	-----	-----	423
H94519	-----	-----	-----	-----	-----	
R74593 corr.	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	293
Consensus	ACTCCTGCAA	TAACTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	490
Translation	S C N	N F I	Y G G C	R G N	K N S	145

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	343
Consensus	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	540
Translation	Y R S E	E A C	M L R	C F R Q	Q E N	162

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	393
Consensus	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	590
Translation	P P L	P L G S	K V V	V L A	G A V S	179

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	443
Consensus	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	640
Translation	* W C	* S F	S W G A	S M V	L L I	195

R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	GTCTGGAGCT	493
Consensus	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	<u>GTCTGGAGCT</u>	690
Translation	P G G K	E E P	G A C	P A * R	L E L	212

R35464	-----	-----				
N39798	-----	-----				
H94519	-----	-----				
R74593 corr.	TCGGAGATGA	CAAGGGNT				511
Consensus	<u>TCGGAGATGA</u>	CAAGGGNT				708
Translation	R R *	Q G				217

KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO.: 12)

N39798 = Nucleic acid sequence of EST N39798 (SEQ ID NO.: 17)

H94519 = Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16)

R74593 corr. = Corrected version of (SEQ ID NO.: 14) G at b.p. 114

Consensus = Nucleic acid sequence for human bikunin (SEQ ID NO.: 9)

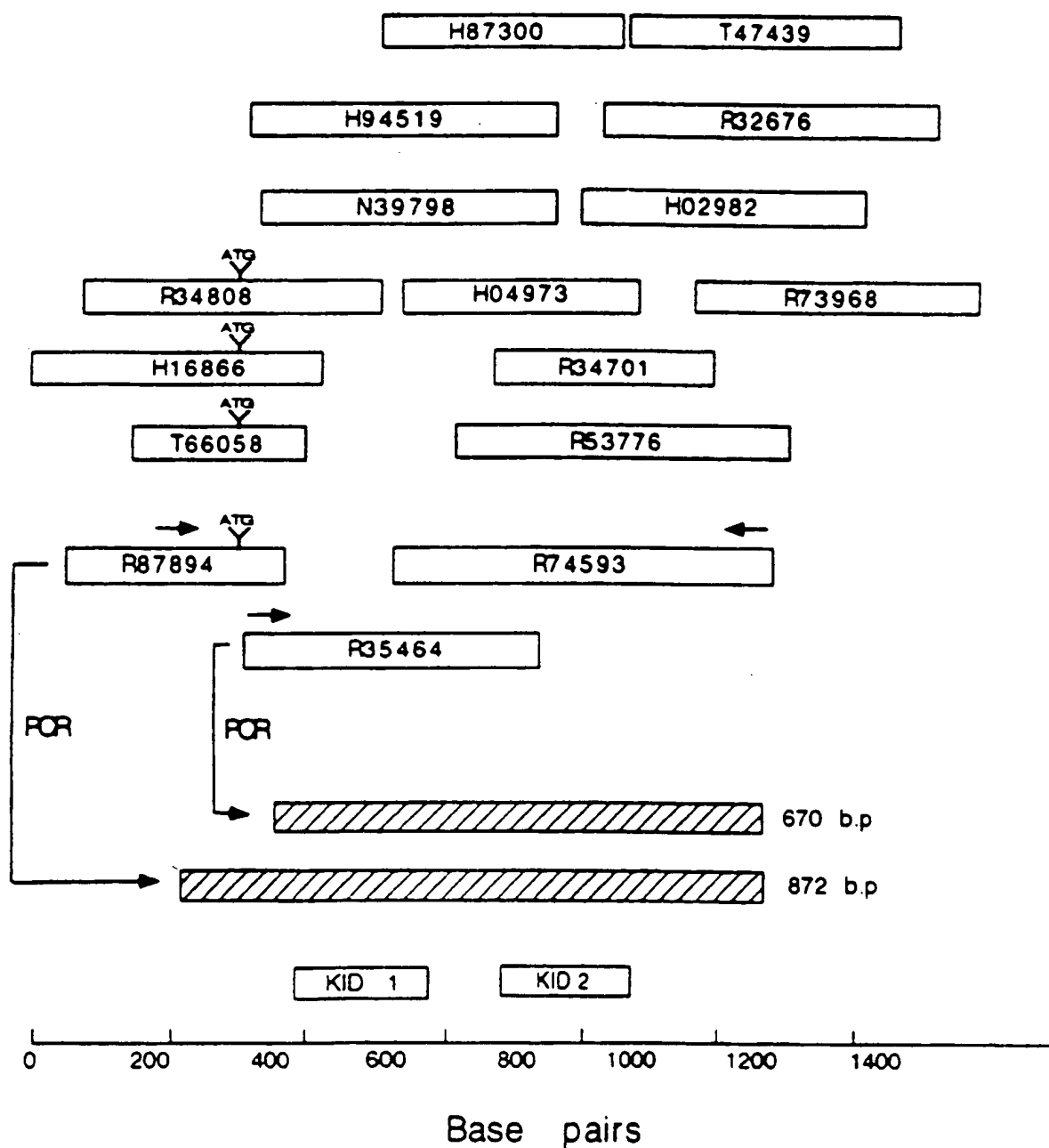
Translation = Amino acid Translation of Consensus (SEQ ID NO.: 10)

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Figure 4 A.

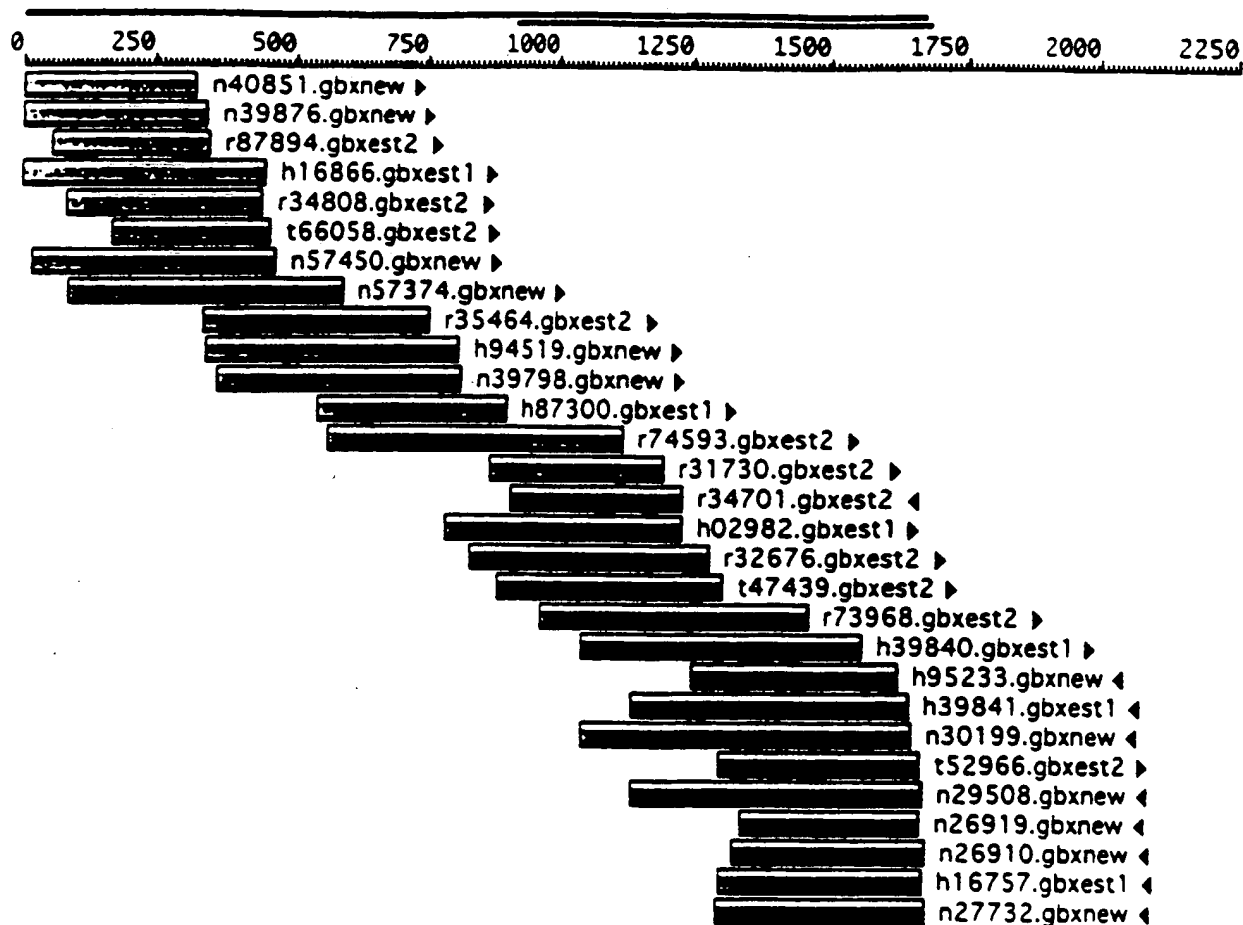
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Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin



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Figure 4B



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Figure 4C

	1	50
BikuninGCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT	
N40851GCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT	
N39876GCCA CCTCCGCGCG TTGGGAGGTG TAGCGCGGCT CTGAACGCGT	
R87894	
H16866GGCGA CCTCCGCGCG TTGGGAGGTG TAGCGCG.CT CTGAACGGGN	
R34808	
T66058	
N57450T TAGCGCGGCT CTGAACGCNA	
N57374	
R35464	
H94519	
N39798	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

BB2222T" E168T260

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Figure 4C (Con't)

	5:	100
Bikunin	GNA GGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCCGAGT GAGGAGCAGA	
N40851	NGAGNGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCCGAGT GAGGAGCAGA	
N39876	GCA.GGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCCGAGT GAGGAGCAGA	
R87894 TTGAGTGTNG NAGGCGGCCA GGGCCCGAGT GAGGAGCAGA	
H16866	..ANGGCCG TTGAGTGTCC CAGGCGGC.A GGCEN.GAGT GAGGAGCAGA	
R34808G GAGGAGCAGA
T66058
N57450	GAAGNGGCCG TTGAGTGTCC CAGGCGGCCA GGGCCCGAGT GAGGAGCAGA	
N57374AGA
R35464
H94519
N39798
H87300
R74593
R31730
R34701
HC2982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

BB222T" E F B F 260

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Figure 4C (Con't)

	101				150
Bikunin	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N40851	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N39876	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	NTCCCCACAC	TGAAGGTCCG
R87894	CCCAGGCATC	GCGCGCCGAG	AAGGCCGGGC	GTCCCCACAC	TGAAGGTCCG
H16866	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
R34808	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
T66058
N57450	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
N57374	CCCAGGCATC	GCGCGCCGAG	AAGNC.GGGC	GTCCCCACAC	TGAAGGTCCG
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

BBB-AT-ETBTE60

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Figure 4C (Con't)

	151			200
Bikunin	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
N40851	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
N39876	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
R87894	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
H16866	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
R34808	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
T66058	GGACCCT
N57450	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
N57374	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

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Figure 4C (Con't)

	201	250
Bikunin	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
N40851	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTNTG .AGGGGCTTC	
N39876	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
R87894	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
H16866	.GGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
R34808	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTNTG GAGGGGCTTC	
T66058	CGGCACCTGA ACGCGAGGCG CTCCATTGCG .GTGCGTGTG NAGGGGCTTC	
N57450	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
N57374	CGGCACCTGA ACGCGAGGCG CTCCATTGCG CGTGCGTTTG .AGGGGCTTC	
R35464	
H94519	
N39798	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

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Figur 4C (C n't)

	251	300
Bikunin	CCGCACCT G ATCGCGAGAC CCCAACGGCT GGTGG CGTC GC TG CGCG	
N40851	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
N39876	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
R87894	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TN.CGCG	
H16866	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTNG.CGTC GC.TGGCGCG	
R34808	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGGGGCT GC.TG.CGCG	
T66058	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CGCG	
N57450	CCGCACCT.G ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GCCTG.CGCG	
N57374	CCGGAACCTG ATCGCGAGAC CCCAACGGCT GGTGG.CGTC GC.TG.CGCG	
R35464	
H94519	
N39798	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

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Figure 4C (C n't)

	30:	350
Bikunin	TC TCGGCTG AGCT GGCCA TGGCGCANT GTTGC GGGC T GAGGC GC	
N40851	TC.TCGGCTG AGCT.GGNCA TGTCG	
N39876	TC.TCGGCTG AGCT.GGCCA TGGCGCACT. G.TCGCGNGC T.GAGGC.G	
R87894	TC.TCGGCTG AGCTTGGCCA TGGCGCANT. GTTNC.GGGC T.NAGGC.GG	
H16866	TTCTCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG	
R34808	TCTTCGGCTG AGCTGGGCCA TGGCGCANTT GTTGC.GGGC T.GAGGC.GG	
T66058	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG	
N57450	TC.TCGGCTG AGCT.GGCCA TGGCGCANT. GGTGC.GGGC TTGAGGC.GG	
N57374	TCCTCGGCTG AGCT.GGCCA TGGCGCANT. GGTGCCGNGC T.GAGGCCGG	
R35464GGCCGG	
H94519	
N39798	
H87300	
R74593	
R31730	
R34701	
H02982	
R32676	
T47439	
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

09218913 122298

Figure 4C (Con't)

35: 400

Bikunin AC GG CG TTTCTCG CC TGCTGGG A TCGCT GC T CCTCTCT
R87894 ACG.

H16866 AC..CGNCST TTTCTCTCG. CCTTGCTGGG ATTGCTTGC TTCTNTCTG
R34808 ACGCGGNCG. .TTTTTTCGN CCTTGCTGGG ATTGCTTGC TTCTNTCTG
T66058 ...CGGNCG. .TTTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.
N57450 ANN.NGCCG. .TTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT.
N57374 AG..GGCCGG. .TTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCTG
R35464GTCTG. .TTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCT.
H94519 .GCNGCGCG. .TTTNTCG. CN.TGCTGGG A.TCGCT.GC A.CCTCTCT.
N39798CTGGG ANTGGCT.GC T.CCTCTCT.
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

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Bikurin	G G G G T C C T G	G . C G G C C G A	C C G A G A A C G	C A G C A T C C	A C G A C T T C T
H168866	G G G G T T C C T G	G G . C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A A G A A T T T T T
R34808	G G G G T T C . T G	G G G N G G C C G A	N C G A . G A A C G	C A A G C A . T T C	A C G A . T T T
T66058	G G G G . T C C T G	G . . C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A C G A N T T . C T
N57450	G G G G . T C C T G	G . . C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A C G A C T T . C T
N57374	G G G G . T C C T G	G . . C G G C C G A	N C G A A G A A N G	C A . G C A A T C C	A N G A A T T N C T
R35464	G G G G . T C C T G	G . C C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A C G A C I T . C T
H94519	G G G G . T C G N G	G . . C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A C G A C T T . C T
N39798	G G G G . T C C T G	G . . C G G C C G A	C C G A . G A A C G	C A . G C A . T C C	A C G A C T T . C T
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

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Figure 4C (C n't)

	451		500
Bikunin	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG CCTC CATGCCTA G
H16866	GCC		
T66058	TCCTGGTGT	CGAAGG	
N57450	GCCTGGTGT	CGAAGGT GG	TGGGCAG
N57374	GCCTGGTGT	CGAAGTTGG	TGGGCANATT CCGGGCCTT CATGNCTAAG
R35464	GCCTGGTGT	CGAAGGT GG	TGGGCAGATT CCGGG CCTC CATGCCTA G
H94519	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG CCTC CATGCCTA G
N39798	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG CCGGG CCTC CATGCCTA G
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

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Figure 4C (Con't)

	501		550
Bikunin	G TGGT GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT ATG		
N57374	GTTGGTGGT ANAATGTNAA TTAANGATTC TTGCAACTGT TTGTGTNATT		
R35464	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H94519	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
N39798	G.TGGT.GGT ACAATGTCAC TGACGGATCC TGCCAGCTGT TTGTGT.ATG		
H87300		
R74593		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		

	551		600
Bikunin	GGGGCTGTGA CGGAAACA GCAATAATTA CCTGACCAAG GA GGAGTGC		
N57374	GGGGCTNTTA AACCGAAANA .CAATAATNA CCTGACCAAA GAAGNAAT..		
R35464	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H94519	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
N39798	GGGGCTGTGA ..CGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTGC		
H87300	GATTCGGCAC AGGGGAAACA GCAATAATTA CCTGACCAAG GA.GGAGTNC		
R74593 GCAATAATTA CCTGACCAAG GA.GGAGTGC		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		

Bikunin "CTGTGTA"

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Figure 4C (Con't)

	601		650
Bikunin	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
R35464	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
H94519	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
N39798	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
H87300	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
R74593	CTCAAGAAAT GTGCCACTGT CACAGAGAAT GCCACGGGTG ACCTGGCCAC		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		
	651		700
Bikunin	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
R35464	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
H94519	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
N39798	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
H87300	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
R74593	CAGCAGGAAT GCAGCGGATT CCTCTGTCCC AAGTGCTCCC AGAAGGCAGG		
R31730		
R34701		
H02982		
R32676		
T47439		
R73968		
H39840		
H95233		
H39841		
N30199		
T52966		
N29508		
N26919		
N26910		
H16757		
N27732		

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Figure 4C (C n't)

	701	750
Bikunin	ATTCT GAAG ACCACTCCAG CGATATGTT	CAACTAT G AAGAATACTG
R35464	ATTCTTGAAG ACCACTTCAG CGATATGTTT	CAANTATTGN AAGAATAATT
H94519	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
N39798	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
H87300	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
R74593	ATTCT.GAAG ACCACTCCAG CGATATGTT.	CAACTAT..G AAGAATACTG
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732
	751	800
Bikunin	CACCGCCAA CGCAGT CAC TGGGCC TTG CCGTG CAT	CCTT CCCAC
R35464	GCACCGNCAA CGNATT	
H94519	GCACCGCCAA CGCATT.CAC TGGGCC..TG C.GTG.CAT.	CCTT.CCCAC
N39798	.CACCGCCAA CGCAGT.CAC TGGGGCCTTG C.GTGGAAAT.	CCTTCCCAC
H87300	.CACCGCCAA CGCAGTNCAC TGGGCC.TTG C.GTGGCATN	CCTT.CCCAC
R74593	.CACCGCCAA CGCAGT.CAC TGGGCC.TTG CCGTG.CAT.	CCTT.CCCAC
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

362221" E T B F 260

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Figure 4C (C n't)

801 850

Bikunin GCTGGTACTT T GACGTGGA GA GGAAGTC CTG CAATAA CTTCATCTAT
H94519 GCTGGTACTT T.GNCGT
N39798 GCTGGNAATT TNGACGTTGA GAAGGAAC
H87300 GCTNGTACTT T.GACGTGGA GA.GGAAGTC CTGGCAATAA CTTCATCTAT
R74593 GCTGGTACTT T.GACGTGGA GA.GGAAGTC CTG.CAATAA CTTCATCTAT
R31730
R34701
H02982GA GA.GGAAGTC CTG.CAATAA CTTCATCTAT
R32676G ATTC..GGAA
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

851 900

Bikunin GGAGGCT GC CGGGGCAAT AAGAACAG C TACCGCTC T GAGGAGGCCT
H87300 GGAGGCTTGC CGGGGCAATN AAGAACAGNT TACCGCTCTT TAGGAGGCCT
R74593 GGAGGCT.GC CGGGGCAAT. AAGAACAG.C TACCGCTC.T GAGGAGGCCT
R31730G.C TACCGCTC.T GAGGAGGCCT
R34701
H02982 GGNGGCT.GC CGGGG.AAT. AAGAACA.NC TACCGCTC.T GAGGAGGCCT
R32676 CGAGGA..GC CGGGGCAAT. AAGAACAG.C TACCGCTC.T GAGGAGGCCT
T47439NGGCCT
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

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Figure 4C (Con't)

	901	950
Bikunin	GCA TGCTC CGGTGCTTCC GC	CA GCAGGA
H87300	.GCA.T....	
R74593	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R31730	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R34701TTCC GC.....	.CAAGCAGGA
H02982	.GCG.TGCTC CGGTGCTTCC GCTGTGTSTT CTCTTCCAGG	CCA.GCAGGA
R32676	.GCA.TGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
T47439	TGCAGTGCTC CGGTGCTTCC GC.....	.CA.GCAGGA
R73968	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

	951	1000
Bikunin	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG CGGGGC
R74593	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGGCGGGGC
R31730	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R34701	AAANTCCTCC CCTCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGC
H02982	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R32676	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
T47439	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R73968CGGGGC
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

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Figure 4C (Con't)

	1001	1050
Bikunin	TGTT CGTGA TGGTGTGAT CC T CTTC TGGG AGCCT CC ATGGTC	
R74593	TGTT CGTGA TGGTGTGAT CCTT..TTCC TGGGGAGCCT CC.ATGGTC	
R31730	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGGGAGCCT CC.ATGGTC.	
R34701	TGTT.CGTGA TGGTGTGAT CCTCTCTCC CGGG.AGCCT CCCATGGTCC	
H02982	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTN.	
R32676	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.	
T47439	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.	
R73968	TGTT.CGTGA TGGTGTGAT CC.T.CTTC TGGG.AGCCT CC.ATGGTC.	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

	1051	1100
Bikunin	TACC TGAT CCGGGTGGCA CGGAGG AAC C AGG AGCG TGGCCTGGCG	
R74593	TACC.TGAT CCGGGTGGCA AGGAGG.AAC C.AGG.AGCG TGGCCTGGCG	
R31730	TACC.TGAT CCGGGTGGCA CGGAGGGAAC C.AGGAGCG TGGCCTGGCG	
R34701	TACCCTGAT CCGGGTGGCA CGGAGG.AAC CCAGG.ANCG TGGCCTGGCG	
H02982	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGGAGCG TGGCCTGGCG	
R32676	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGGAGCG TGGCCTGGCG	
T47439	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGG.AGCG TGGCCTGGCG	
R73968	TACC.TGAT CCGGGTGGCA CGGAGG.AAC C.AGG.AGCG TGGCCTGGCG	
H39840GGG.AAC C.AGG.AGCG TGGCCTGGCG	
H95233	
H39841	
N30199GAGGAACC C.ANG.AGCT TGGCCTGGCG	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

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Figure 4C (Con't)

	1101		1150
Bikunin	ACCG TCT G GAGCTCCGGA GATGACAAGG	AGCAGCTGG	TGAAGAAC
R74593	ANCG.TCT.G GAGCTCCGGA GATGACAAGG	GNT	
R31730	ACCG.TCTGG GAGCTCCGGA GATGACAAGG	GAGCAGCTGG	GTGAAGAAC.
R34701	ACCG.TCT.G GAGCTCCGGA GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.
H02982	ACCG.TCTNG GAGCTCCGGA GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.
R32676	ACCG.TCTGG GAGCTCCGGA GATGACAAGG	GAGCAGCTGG	.TGAAGAAC.
T47439	ACCG.TCT.G GAGCTCCGGA GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.
R73968	ACCG.TCT.G GAGCTCCGGA GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.
H39840	ACCGTCT.G GAGCTCCGGA GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.
H95233
H39841
N30199	ACCG.TCT.G GAGCTCCGGA GATNACAANG	.AGCAGCTGN	.TGAAGAACC
T52966
N29508
N26919
N26910
H16757
N27732

	1151		1200
Bikunin	ACATATGT C CTGT GACCG CCCTGT CGC C	AAGAGG A CT	GGGGAA
R31730	ACATATGTTT CTGTTGACCG NCCTGTTCCG	C.AAGAGG.A	TGGGGGAA.
R34701	ACATATGT.C CTGT.GACCG CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.
H02982	ACATATGT.C CTGT.GACCG NCCTGTTCCG	C.AAGAGG.A	CTNGGGGAAA
R32676	ACATATGTTT CTGTTGACCG CCCTGTTCCG	C.AAGAGGGA	NTGGGGGAA.
T47439	ACATATGT.C CTGT.GACCG CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.
R73968	ACATATGT.C CTGT.GACCG CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.
H39840	ACATATGT.C CTGT.GACCG CCCTGT.CGC	C.AAGAGG.A	CT.NGGGAA.
H95233
H39841C. CCCTGT.CGC	CCAAAAGG.A	CT.GGGGAA.
N30199	ACATATGT.C CTGT.GACCG CCCTNT.CGC	C.AAGAGG.A	CT.GGGNAAA
T52966
N29508CC. CCCTNT.CGC	C.AAGAGG.A	CT.GGG.AA.
N26919
N26910
H16757
N27732

0021891-12299

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Figure 4C (C n't)

1201 1250
Bikunin GGGAGGGG AGACTAT G TGT GA GCT TTTTTT AA A TAGA GG
R31730 .GGGAGGGG A
R34701 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TA
H02982 GGGAGGGG. AGACTAT.G. TGTGA.GTT TTTTTT..AA ANTAG
R32676 GGGAGGGG. AGANTATTGT TGTGA.GNT TTTTTTAAA ATTAGGAGGG
T47439 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
R73968 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
H39840 .GGGAGGGG. AGACTAT.G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
H95233
H39841 .GGGAGGGG. AAACNAT.G. TGT.GAACCT TTTTTT.AAA A.TAGA..GG
N30199 .GGGAGGGG. AGACTAT.G. TGT.AA.GCT TTTTTT..AA A.TAGA..GG
T52966
N29508 .GGGAGGGG. AGACTA..G. TGT.GA.GCT TTTTTT..AA A.TAGA..GG
N26919
N26910
H16757
N27732

1251 1300
Bikunin GATTGACTC GCATTTC A GT GATC A TTAGGG CT GAGGTCTGTT
R32676 GNTTGANTTC GGGNTTTTNA GTTGATCCAT TTAGGGGGNT GAG
T47439 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
R73968 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
H39840 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
H95233A. TTAGGG..CT GAGGTCTGTT
H39841 GATTGACTC..GGATTTC.A GT.GATC.A. TTAGGG..CT GAGGTCTGTT
N30199 GATTGACTC..GGATTTCGA GT.GATC.A. TTAGGG..CT GAGGTCTGTT
T52966
N29508 GATTGACTC..GGATTTC.A GT.GATCNA. TTAGGG..CT GAGGTCTGTT
N26919
N26910
H16757
N27732

1301 1350
Bikunin TCTCTGGGAG GTAGGACGGC TGCTTCC TG G TC TGGCA GGGATGGG
T47439 TCTCTNGGAG GTAGGACGA
R73968 TCTCTGGGAG GTAGGACGGC TGCTTCC TG GGTCTTGGCA .GGGATGGG
H39840 TCTCTGGGAG GTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.
H95233 NCTCTGGGAG NTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.
H39841 TCTCTGGGAG GTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.
N30199 TCTCTGGGAG GTAGGACGGC TGCTTCC TG G.TC.TGGCA .GGGATGGG.
T52966G.TC.TGGCA .GGGATGGG.
N29508 TCTCTGGGAG GTAGGACGGC TGCTTCA TG G.TC.TGGCA .GGGATGGG.
N26919
N26910
H16757G.TC.TGGCA .GGGATGGG.
N27732GGCTG GGTCTGNCNA AGGNATGGG

00218913-123998

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Figure 4C (Con't)

1351 1400
 Bikunin TTTG CTTTG G AAATCCTC T AGGAGGCT CCTCCT CGC ATGG CC TG
 R73968 TTTG.CTTTG GGAAATCCTC TTNGGAGGCT CCTCCTCGC ATGGGCCCTG
 H39840 TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG
 H95233 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 H39841 TTTG.CTTTG G.AAANCNC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N30199 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTCGC ATGG.CC.TG
 T52966 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N29508 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N26919GAGGCT CCTCCT.CGC ATGG.CC.TG
 N26910CTTTT GNAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 H16757 TTTGCCCTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N27732 TTTG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG

1401 1450
 Bikunin CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTC
 R73968 CAGT.CTNGG CAGCANCCCC CGAGTTTTTT TCGCTCGCTG ATCCGATTTC
 H39840 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H95233 CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H39841 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC
 N30199 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 T52966 CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N29508 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N26919 CAGT.CTTGG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC
 N26910 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTC
 H16757 CAGTNCT.GG CAGCAGACCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N27732 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC

1451 1500
 Bikunin TTT CCTCCA GGTAG AGT TTTC TTTC CITATGTTGA ATTCCATTGC
 R73968 TTTTCTTCCA GGTAAAGAATT TTTCCTTT
 H39840 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 H95233 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 H39841 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ANTCCATTGC
 N30199 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 T52966 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 N29508 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 N26919 TTT.CCNCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 N26910 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC
 H16757 TTTACCCCA GGTAG..AGT TTTCCTTTGN CITATGTTGA ATTCCATTGC
 N27732 TTT.CCTCCA GGTAG..AGT TTTC.TTTC. CITATGTTGA ATTCCATTGC

B6222T 13298

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Figur 4C (Con't)

1501 1550

Bikunin CTCTTTT CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT GT
H39840 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTTGT
H95233 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
H39841 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
N30199 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
T52966 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
N29508 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
N26919 CTCTTTT.CN CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
N26910 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
H16757 CTCTTTTACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
N27732 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT

1551 1600

Bikunin CTGATTATG G TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
H39840 CTGATTATG GGTTTTTTT AAGTAT
H95233 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
H39841 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
N30199 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
T52966 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
N29508 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
N26919 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
N26910 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
H16757 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
N27732 CTGATTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT

1601 1650

Bikunin CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
H95233 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAA
H39841 CTGAAAGAAG GAAAGTAAAN TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N30199 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
T52966 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N29508 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N26919 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N26910 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
H16757 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N27732 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC

1651 1689

Bikunin CTTTAG AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
H39841 CTTTAA.
N30199 CTTTAG.AAT AAA
T52966 CTTTAGGAAT NAAAAHAAAA AAGGOTS
N29508 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AA
N26919 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA A
N26910 CTTTAG.AAT AAATTCAGC ATGTGCTTTC AAAAAA
H16757 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAA
N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

09218913 "122298

FIGURE 4D

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EST c nsens MLRAEADGVS RLLGSLLLSG VLAADRERSI HDFCLVSKVV GRCRASMPRW 50
EST consens WYNVTDGSCQ LFVYGGCDGN SNNYLTKEEC LKKCATVTEN ATGDLATSRN 100
EST consens AADSSVPSAP RRQSEDHSS DMFNYEEYCT ANAVTGPCRA SFPRWYFDVE 150
EST consens RNSCNFIYG GCRGNKNSYR SEEACMLRCF RQENPPLPL GSKVVVLAGL 200
EST consens FVMVLLFLG ASMYLIRVA RRNQERALRT VWSSGDDKEQ LVKNITYVL 248

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FIGURE 4E

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cDNA		ACC	3
translation		T	-47
cDNA	TGATCGCGAG ACCCCAACGG CTGGTGGCGT CGCCTGCGCG TCTCGGCTGA	53	
translation	S R D P N G W W R R L R V S A E	-30	
cDNA	GCTGGCCATG GCGCAGCTGT GCGGGCTGAG GCGGAGCCGG GCGTTTCTCG	103	
translation	L A M A Q L C G L R R S R A F L A	-13	
cDNA	CCCTGCTGGG ATCGCTGCTC CTCTCTGGGG TCCTGGCGGC CGACCGAGAA	153	
translation	L L G S L L L S G V L A A D R E	4	
cDNA	CGCAGCATCC ACGACTTCTG CCTGGTGTCTG AAGGTGGTGG GCAGATGCCG	203	
translation	R S I H D F C L V S K V V G R C R	21	
cDNA	GGCCTCCATG CCTAGGTGGT GGTACAATGT CACTGACGGA TCCTGCCAGC	253	
translation	A S M P R W W Y N V T D G S C Q L	38	
cDNA	TGTTTGTGTA TGGGGGCTGT GACGGAAACA GCAATAATTA CCTGACCAAG	303	
translation	F V Y G G C D G N S N N Y L T K	54	
cDNA	GAGGAGTGCC TCAAGAAATG TGCCACTGTC ACAGAGAATG CCACGGGTGA	353	
translation	E E C L K K C A T V T E N A T G D	71	
cDNA	CCTGGCCACC AGCAGGAATG CAGCGGATTC CTCTGTCCCA AGTGCTCCCA	403	
translation	L A T S R N A A D S S V P S A P R	88	
cDNA	GAAGGCAGGA TTCTGAAGAC CACTCCAGCG ATATGTTCAA CTATGAAGAA	453	
translation	R Q D S E D H S S D M F N Y E E	104	
cDNA	TACTGCACCG CCAACGCAGT CACTGGGCCT TGCCGTGCAT CCTTCCCACG	503	
translation	Y C T A N A V T G P C R A S F P R	121	
cDNA	CTGGTACTTT GACGTGGAGA GGAATCCTTG CAATAACTTC ATCTATGGAG	553	
translation	W Y F D V E R N S C N N F I Y G G	138	
cDNA	GCTGCCGGGG CAATAAGAAC AGCTACCGCT CTGAGGAGGC CTGCATGCTC	603	
translation	C R G N K N S Y R S E E A C M L	154	
cDNA	CGCTGCTTCC GCCAGCAGGA GAATCCTCCC CTGCCCCTTG GCTCAAAGGT	653	
translation	R C F R Q Q E N P P L P L G S K Y	171	
cDNA	GGTGGTTCTG GCGGGGCTGT TCGTGATGGT GTTGATCCTC TTCCTGGGAG	703	
translation	<u>V V L A G L F V M V L I L F L G A</u>	198	
cDNA	CCTCCATGGT CTACCTGATC CGGGTGGCAC GGAGGAACCA GGAGCGTGCC	753	
translation	<u>S M V Y L I</u> R V A R R N Q E R A	204	
cDNA	CTGCGCACCG TCTGGAGCTT CGGAGATGA	792	
translation	L R T V W S F G D	213	

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FIGURE 4F

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cDNA GCACGAGTTG GGAGGTGTAG CGCGGCTCTG AACGCGCTGA GGGCCGTTGA 50
 cDNA GTGTGCGCAGG CGGCGAGGGC GCGAGTGAGG AGCAGACCCA GGCATCGCGC 100
 cDNA GCCGAGAAGG CCGGGCGTCC CCACACTGAA GGTCCGGAAA GCGGACTTCC 150
 cDNA GGGGGCTTTG GCACCTGGCG GACCCTCCCG GAGCGTCGGC ACCTGAACGC 200
 cDNA GAGGCGCTCC ATTGCGCGTG CGCGTTGAGG GGCTTCCCGC ACCTGATCGC 250
 cDNA GAGACCCCA CGGCTGGTGG CGTCGCCTGC GCGTCTCGGC TGAGCTGGCC 300
 cDNA ATGGCGCAGC TGTGCGGGCT GAGGCGGAGC CGGGCGTTTC TCGCCCTGCT 350
 translation M A Q L C G L R R S R A F L A L L -11

cDNA GGGATCGCTG CTCCTCTCTG GGGTCCTGGC GGCCGACCGA GAACGCAGCA 400
 translation G S L L L S G V L A A D R E R S I 7

cDNA TCCACGACTT CTGCCTGGTG TCGAAGGTGG TGGGCAGATG CCGGGCCTCC 450
 translation H D F C L V S K V V G R C R A S 23

cDNA ATGCCTAGGT GGTGGTACAA TGTCCTGAC GGATCCTGCC AGCTGTTTGT 500
 translation M P R W W Y N V T D G S C Q L F V 40

cDNA GTATGGGGGC TGTGACGGAA ACAGCAATAA TTACCTGACC AAGGAGGAGT 550
 translation Y G G C D G N S N N Y L T K E E C 57

cDNA GCCTCAAGAA ATGTGCCACT GTCACAGAGA ATGCCACGGG TGACCTGGCC 600
 translation L K K C A T V T E N A T G D L A 73

cDNA ACCAGCAGGA ATGCAGCGGA TTCCTCTGTC CCAAGTGCTC CCAGAAGGCA 650
 translation T S R N A A D S S V P S A P R R Q 90

cDNA GGATTCTGAA GACCACTCCA GCGATATGTT CAACTATGAA GAATACTGCA 700
 translation D S E D H S S D M F N Y E E Y C T 107

cDNA CCGCCAACGC AGTCACTGGG CTTTGCCGTG CATCCTTCCC ACGCTGGTAC 750
 translation A N A V T G P C R A S F P R W Y 123

cDNA TTTGACGTGG AGAGGAACTC CTGCAATAAC TTCATCTATG GAGGCTGCCG 800
 translation F D V E R N S C N N F I Y G G C R 140

cDNA GGGCAATAAG AACAGCTACC GCTCTGAGGA GGCCTGCATG CTCCGCTGCT 850
 translation G N K N S Y R S E E A C M L R C F 157

cDNA TCCGCCAGCA GGAGAATCCT CCCCTGCCCC TTGGCTCAAA GGTGGTGGTT 900
 translation R Q Q E N P P L P L G S K V V V 173

cDNA CTGGCGGGGC TGTTCTGTAT GGTGTTGATC CTCTTCCTGG GAGCCTCCAT 950
 translation L A G L F V M V L L L F L G A S M 190

cDNA GGTCTACCTG ATCCGGGTGG CACGGAGGAA CCAGGAGCGT GCCCTGCGCA 1000
 translation V Y L I R V A R R N Q E R A L R T 207

cDNA CCGTCTGGAG CTCCGGAGAT GACAAGGAGC AGCTGGTGAA GAACACATAT 1050
 translation V W S S G D D K E Q L V K N T Y 223

cDNA GTCCTGTGAC CGCCCTGTCT CCAAGAGGAC TGGGGAAGGG AGGGGAGACT 1100
 translation V L * 225

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FIGURE 4F (Con't)

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cDNA	ATGTGTGAGC	TTTTTTTAAA	TAGAGGGATT	GACTCGGATT	TGAGTGATCA	1150
cDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
cDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
cDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
cDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
cDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCTGA	1400
cDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
cDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
cDNA	AATAAATTTT	CAGCATGTTG	CTTTCAAAAA	AAAAAAAAAA	AAAA	

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SECRET

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Purification of Placental Bikunin using Superdex 75 Gel-Filtration

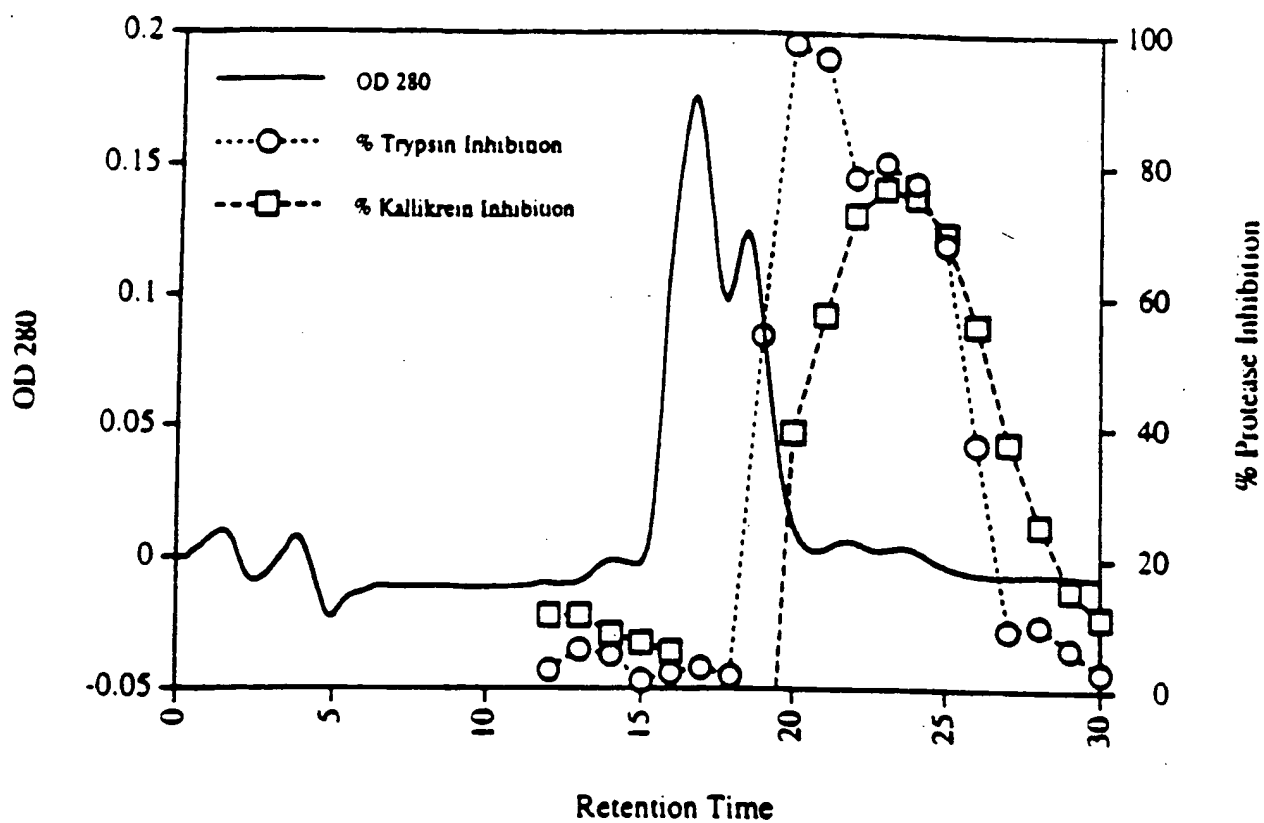


FIGURE 5

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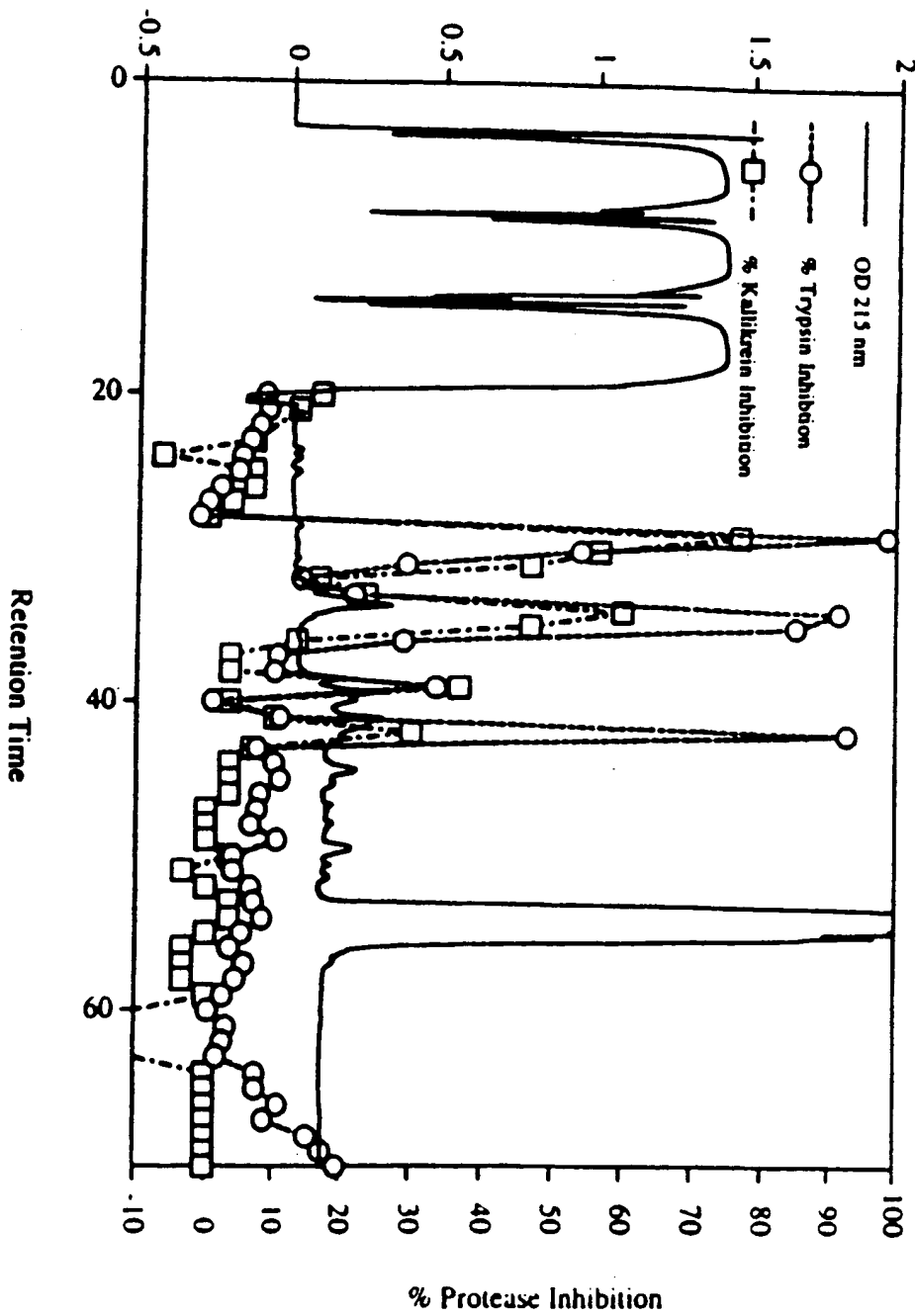


FIGURE 6

Purification of Placental Bikunin using C18 Reverse-Phase Chromatography

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Figure 7

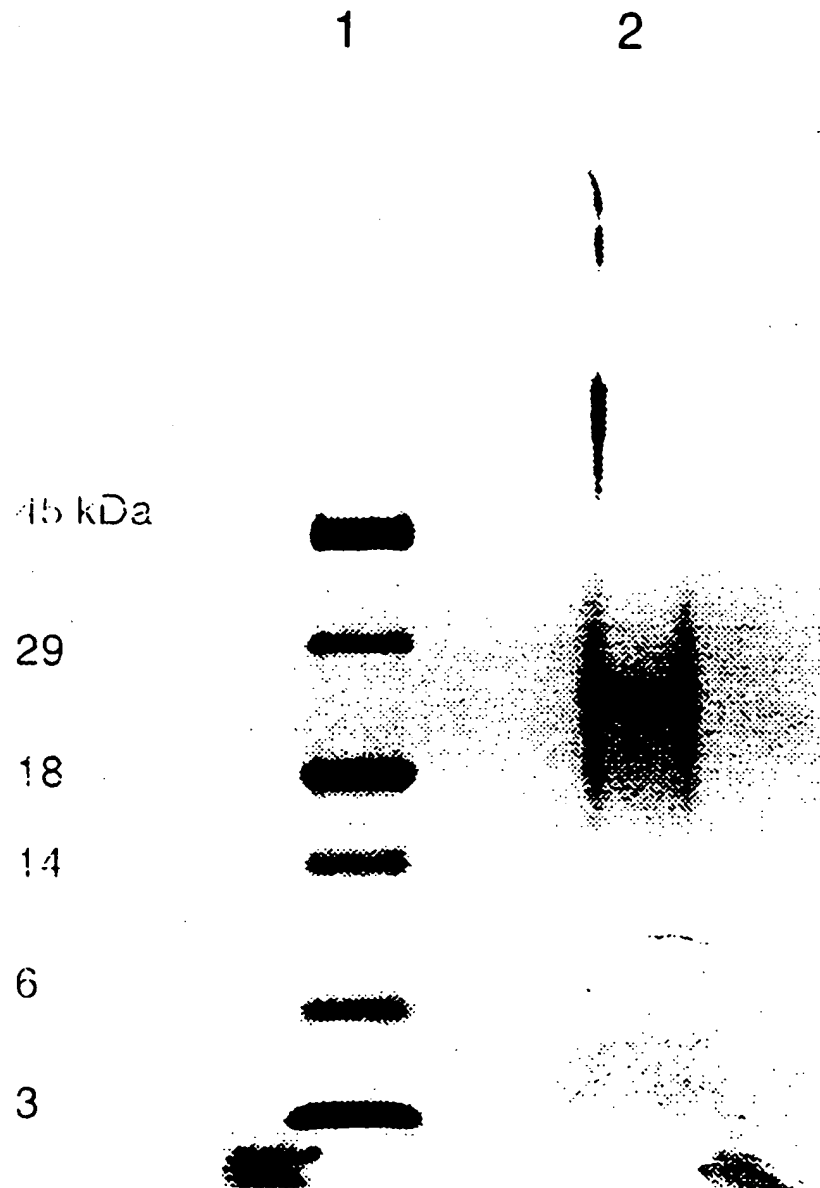


Figure 8A

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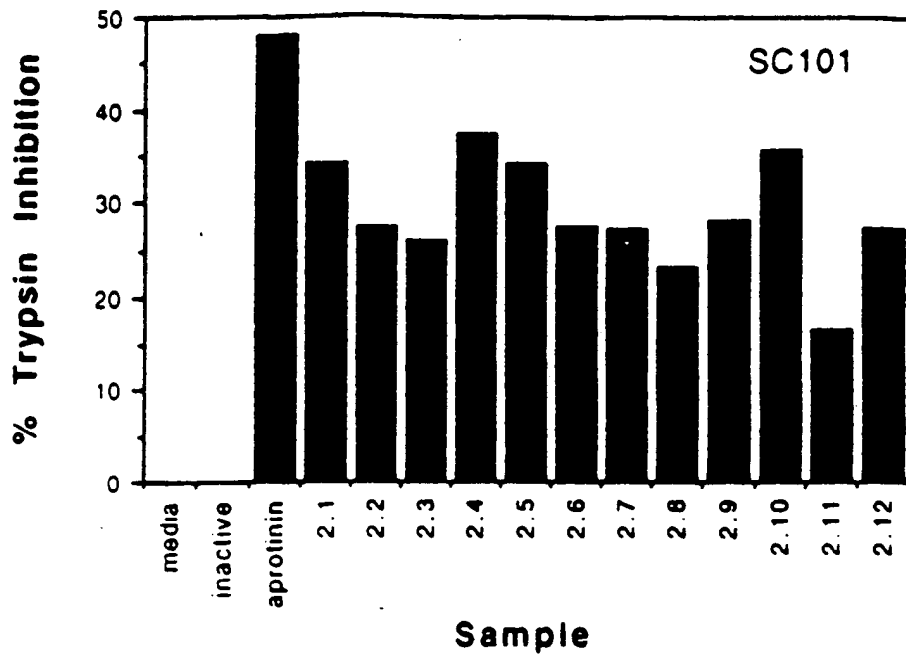
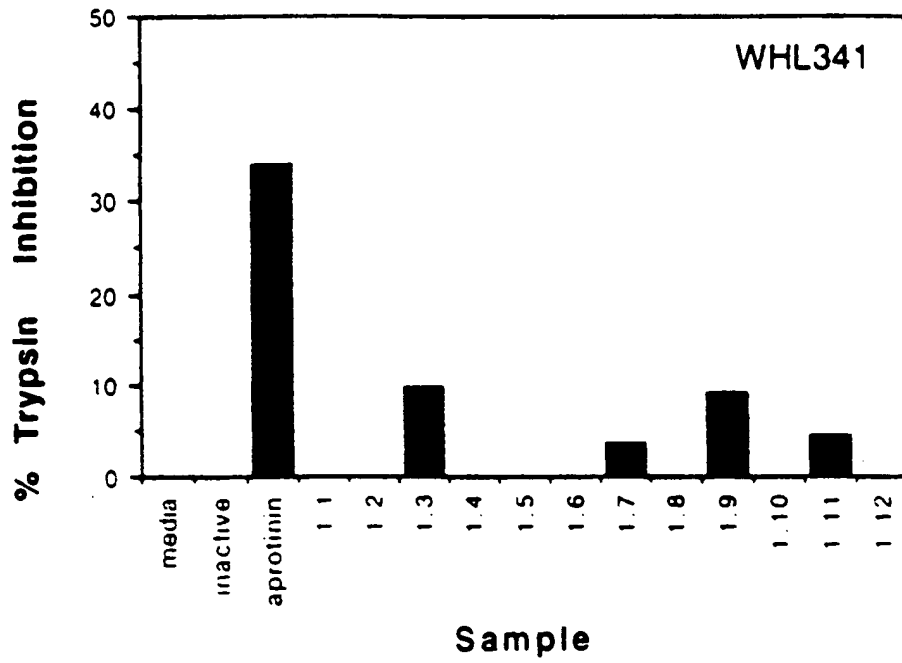


Figure 8B



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Figure 9A

SDS-PAGE

Aprotinin
2.4
2.5

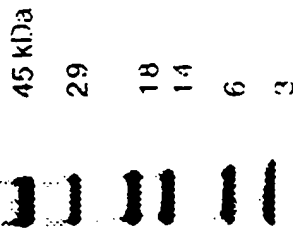
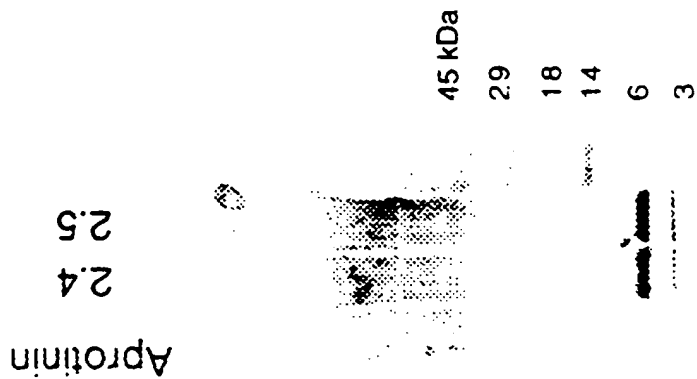


Figure 9B

Western



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Figure 10

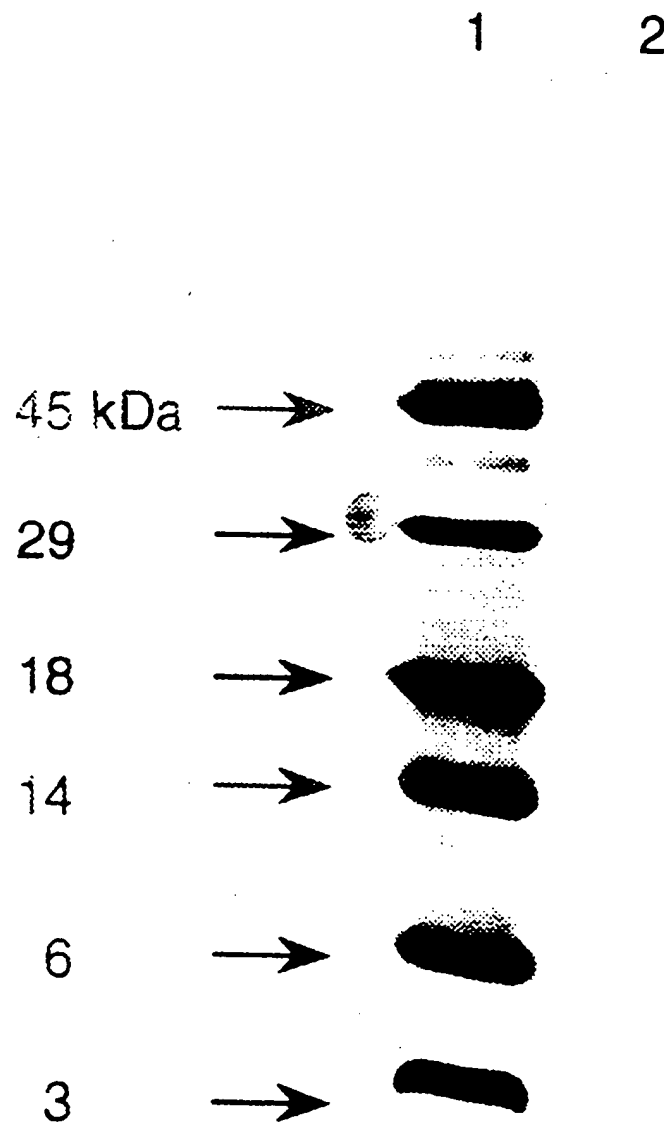


Figure 11A

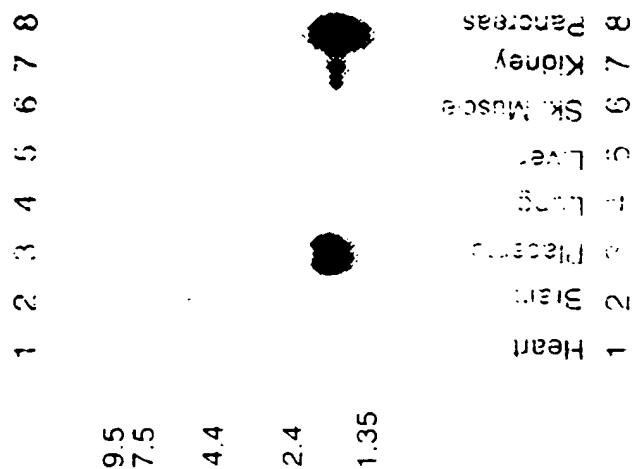
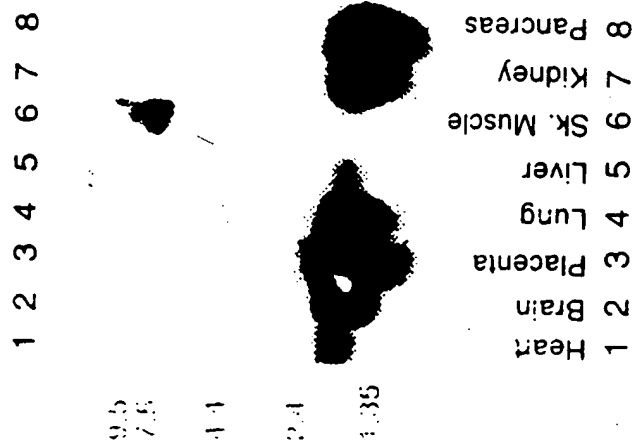


Figure 11B



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Figure 12A

1 2 3 4

45 kDa
29
18
14
6
3



Figure 12B

1 2 3 4

45 kDa
29
18
14
6
3



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Figure 13

1 2

45 kDa

29

18

14

6

3



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Figure 14

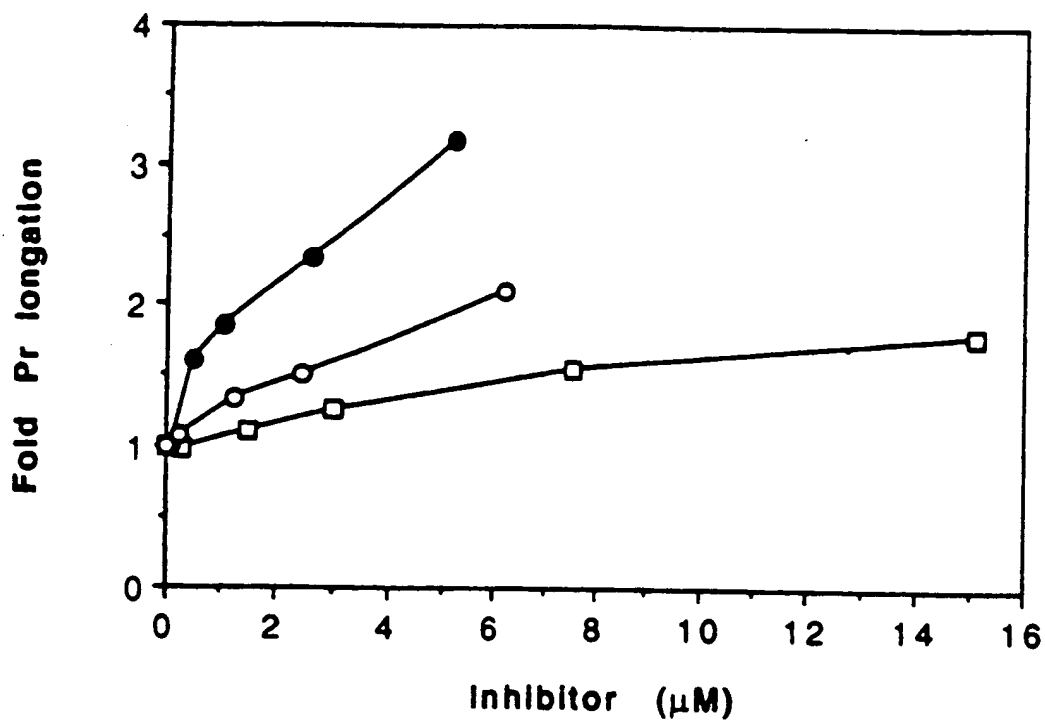
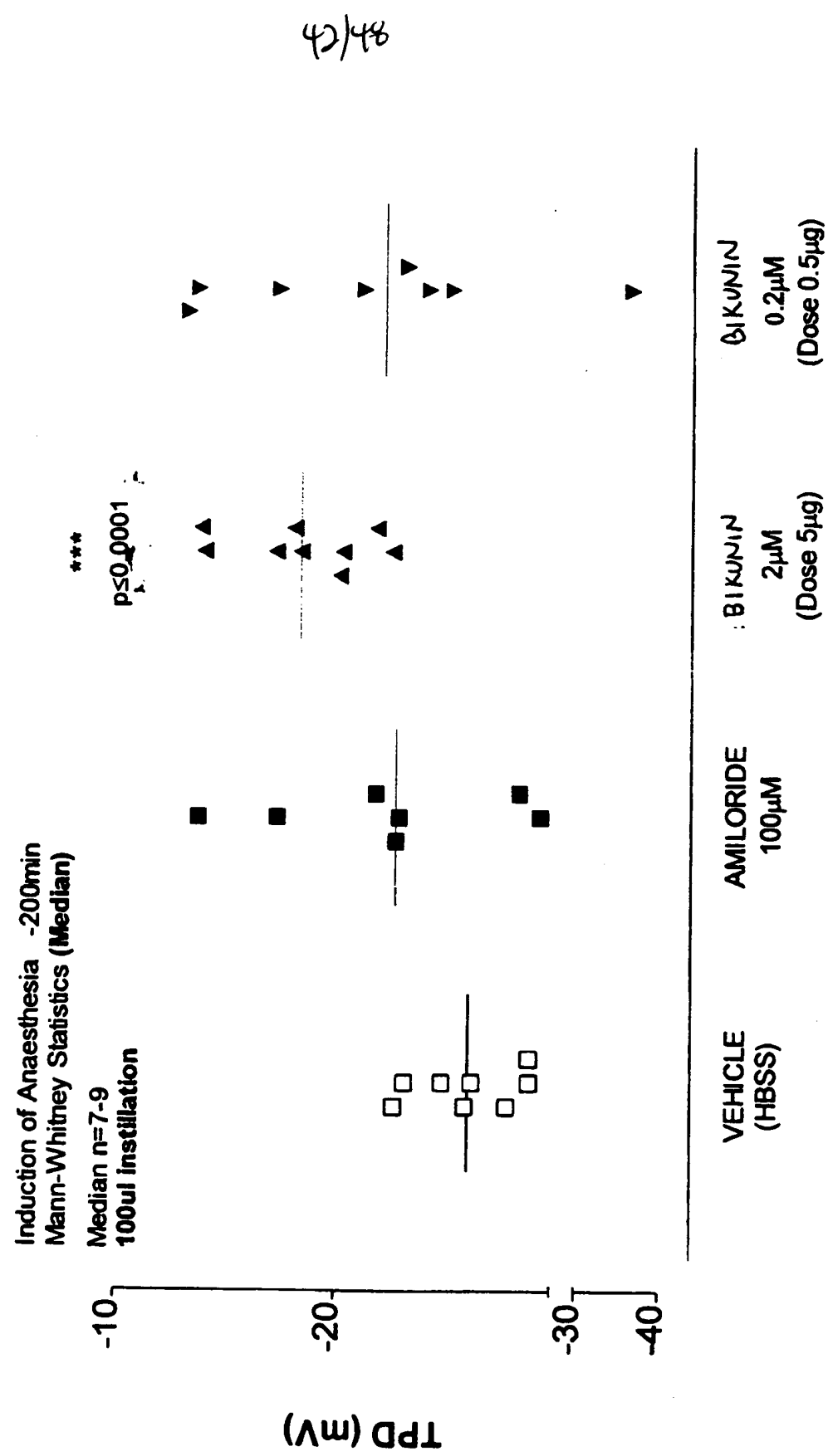


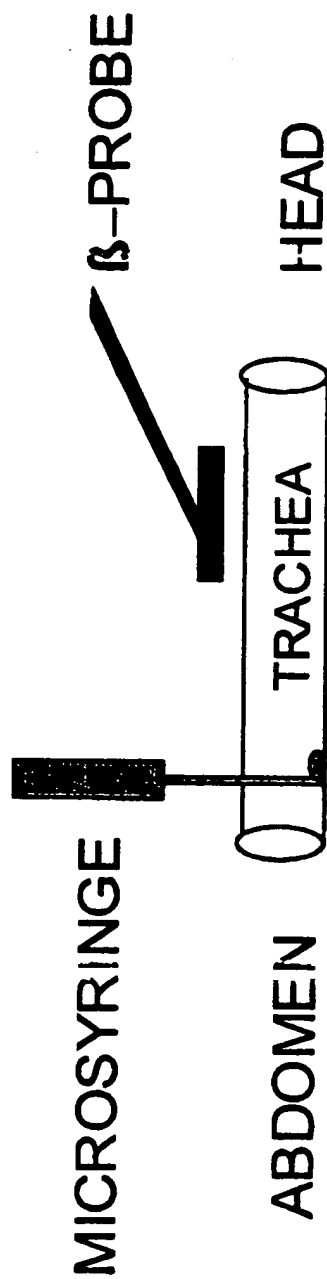
Figure 15 : The effect of BIKUNIN (0.2-2uM) and amiloride (100uM) on tracheal potential difference (TPD) 3 hours post treatment



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Figure 16 (a) : Diagram to show the arrangement of needle and Beta probe.



Longitudinal view

Figure 16 (b) : Counts detected by the probe as the ^{32}P -labeled Saccharomyces cerevisiae are transported along the tracheal mucociliary layer.

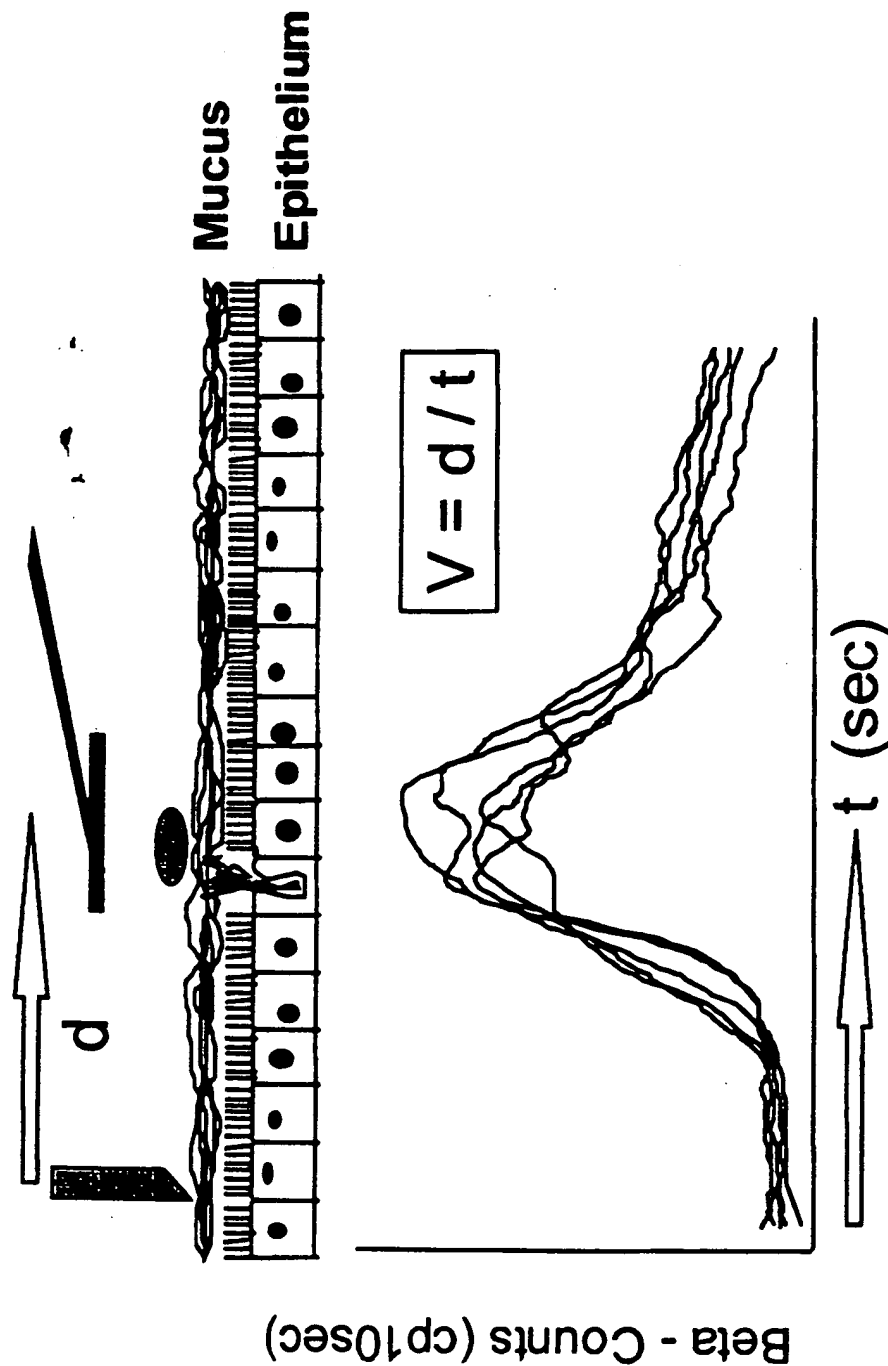


Figure 17 : Short circuit current (Isc) trace to show the action of β IKUNIN (70nM) on sodium dependent current in cultured normal human bronchial epithelial cells in vitro

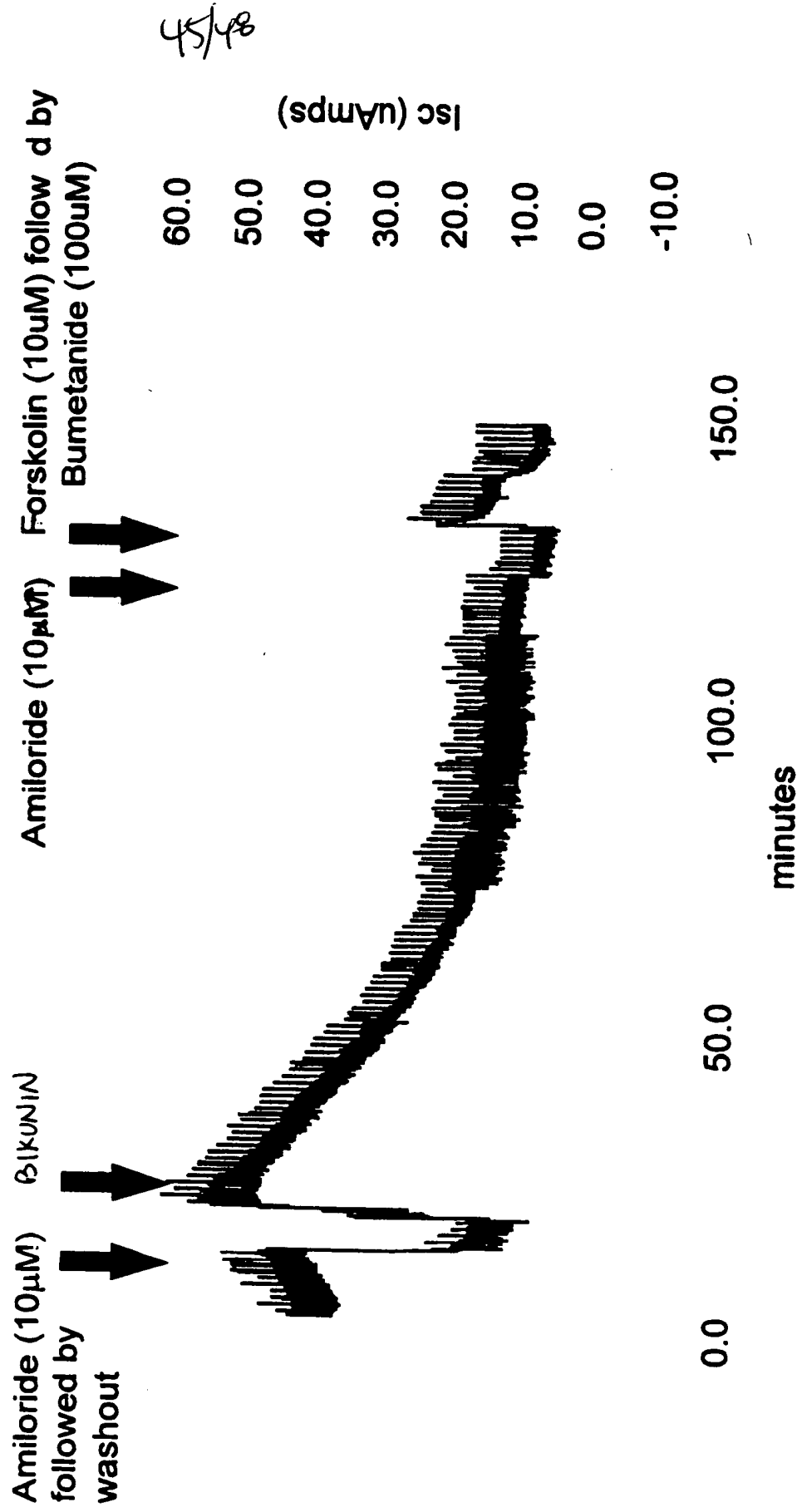


Figure 18 : The effect of a 5 min aerosol of hypertonic saline (14.4%) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig

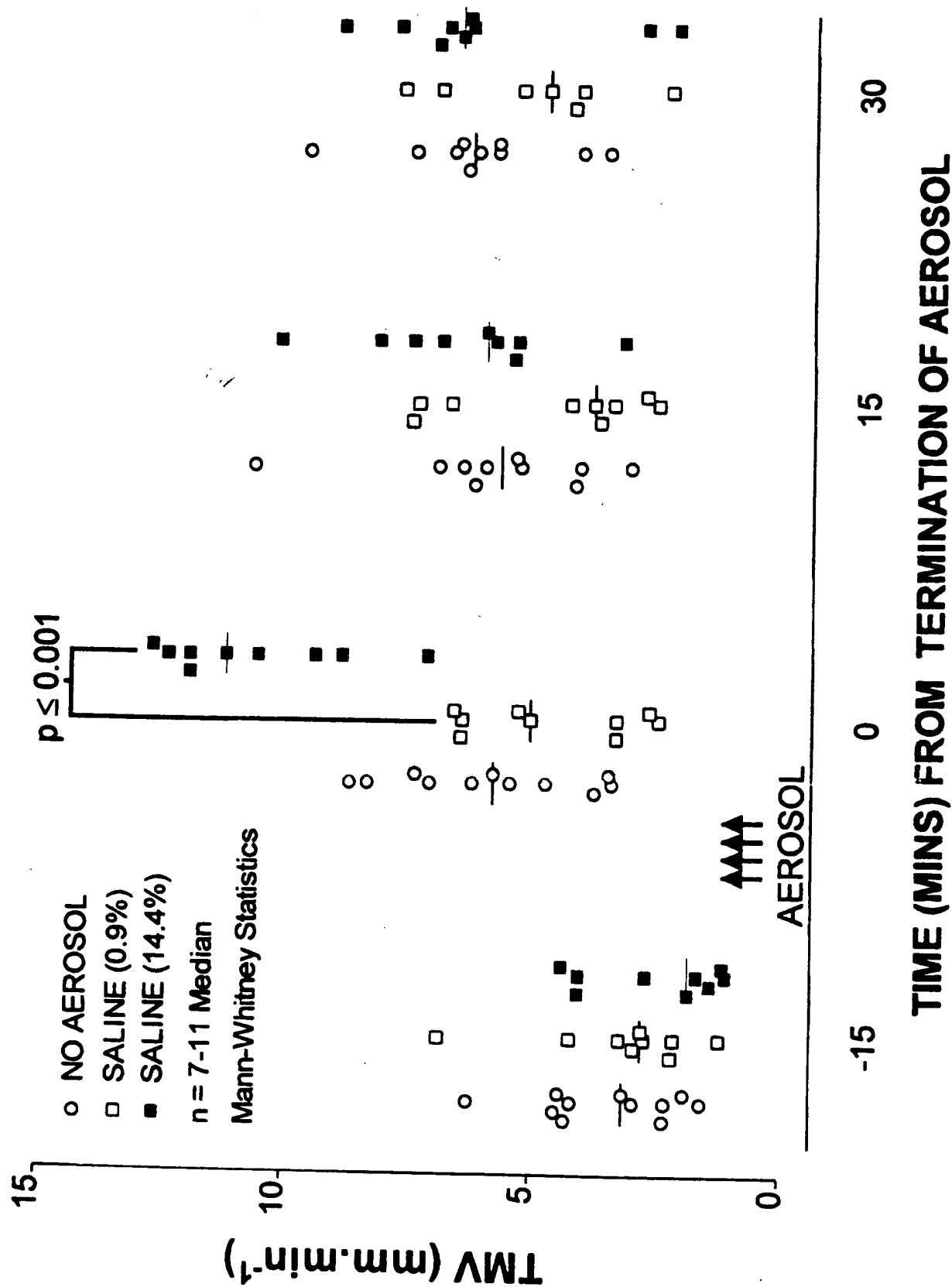
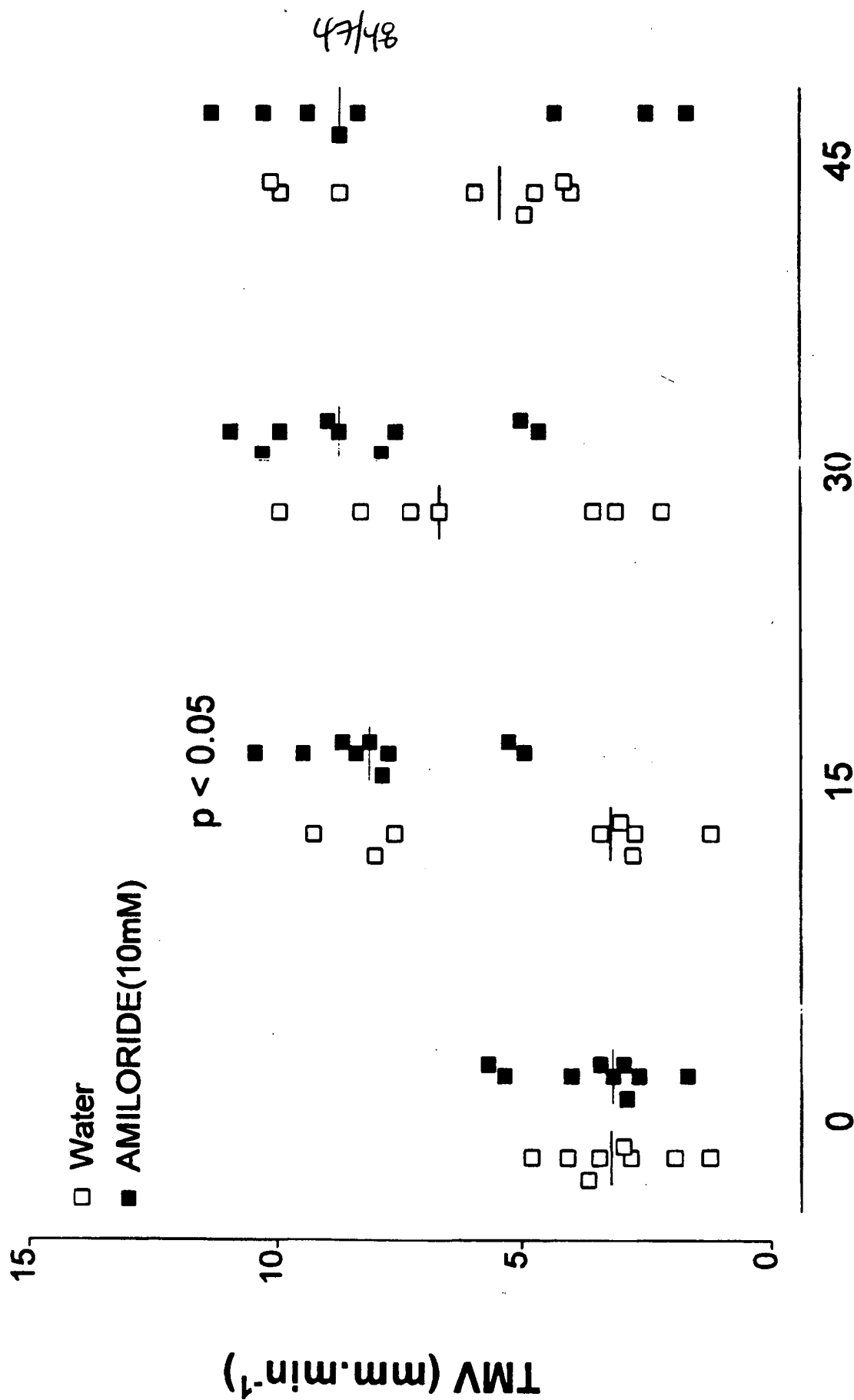


Figure 19 : The effect of a 20 min aerosol of amiloride (10mM) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



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Figure 20 : Short circuit current (Isc) trace to show the action of Aprotinin Double
mucin (0.5-5ug.ml-1) on sodium dependent current in normal human
bronchial epithelial cells in vitro

